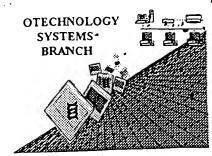# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _0 9 7 5 6 4 8 1 A_

Source: _C I P E_

Date Processed by STIC: _10/ 0 2 / 2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

```
                RAW SEQUENCE LISTING              DATE: 10/02/2001
                PATENT APPLICATION: US/09/756,481A    TIME: 11:48:10

                   Input Set : A:\47506-sequence.txt
                   Output Set: N:\CRF3\10022001\I756481A.raw
```

```
      3 <110> APPLICANT: Mark Marchionni
      4        Michael Jarpe
      5        Ted Ebendal
      7 <120> TITLE OF INVENTION: METHODS FOR TREATING NEUROLOGICAL
      8        INJURIES AND DISORDERS
     10 <130> FILE REFERENCE: 47506 (71095)
     12 <140> CURRENT APPLICATION NUMBER: 09/756,481A
C--> 13 <141> CURRENT FILING DATE: 2001-08-30
     15 <150> PRIOR APPLICATION NUMBER: PCT/US99/15106
     16 <151> PRIOR FILING DATE: 1999-07-02
     18 <150> PRIOR APPLICATION NUMBER: 60/091,791
     19 <151> PRIOR FILING DATE: 1998-07-06
     21 <160> NUMBER OF SEQ ID NOS: 2
     23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 1387
     27 <212> TYPE: DNA
     28 <213> ORGANISM: Artificial Sequence
     30 <220> FEATURE:
     31 <221> NAME/KEY: CDS
     32 <222> LOCATION: (218)...(1288)
W--> 34 <223> OTHER INFORMATION:
     34 <400> SEQUENCE: 1
     35 cccttctcca gggactctgg ctgccagcag ctccgccttt cagatcaatt ctcgaccacc    60
     36 caccttggga ctgccgccca gtcctgccct ctggatcagt ggggtccaga cacgcccccт   120
     37 ccaggacctc aaagcacccc cgacctaagg tcaccagccc actggcccca gacgcagtgg   180
     38 gctccgctga ctctcttgga cacctcctgg gaggaaa atg ctc cct gtc tgc cat   235
     39                                         Met Leu Pro Val Cys His
     40                                         1                   5
     42 cgt ttt tgc gac cac ctc ctc ctc ctg ctc ttg ctg ccc tcg acg acc   283
     43 Arg Phe Cys Asp His Leu Leu Leu Leu Leu Leu Leu Pro Ser Thr Thr
     44                 10                  15                  20
     46 ctg gcc ccc gcg cca gca tcc atg ggc ccc gct gcc gcc ctg ctc cag   331
     47 Leu Ala Pro Ala Pro Ala Ser Met Gly Pro Ala Ala Ala Leu Leu Gln
     48             25                  30                  35
     50 gtt ctt ggg ctt ccc gaa gcg ccc cgg agc gtc ccc aca cac cga cct   379
     51 Val Leu Gly Leu Pro Glu Ala Pro Arg Ser Val Pro Thr His Arg Pro
     52         40                  45                  50
     53 gtg cct cct gtc atg tgg cgc cta ttc cgt cgc cgt gac ccc cag gag   427
     54 Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp Pro Gln Glu
     55 55                  60                  65                  70
     57 gcc aga gtg gga cgc cct ctg cgg cca tgc cac gtg gag gaa cta ggg   475
     58 Ala Arg Val Gly Arg Pro Leu Arg Pro Cys His Val Glu Glu Leu Gly
     59                 75                  80                  85
     61 gtc gcc gga aac att gtg cgc cac atc ccc gac agc ggt ctg tcc tcc   523
     62 Val Ala Gly Asn Ile Val Arg His Ile Pro Asp Ser Gly Leu Ser Ser
     63                 90                  95                  100
```

Handwritten annotations: Does Not Comply / Corrected Diskette Needed

Handwritten note: A 213 response of "Artificial Sequence" requires an explanation or description in field 223

Handwritten circled: Errored

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

```
65   agg ccc gca caa ccc gcc agg acc tcg ggg ctg tgc ccc gag tgg aca       571
66   Arg Pro Ala Gln Pro Ala Arg Thr Ser Gly Leu Cys Pro Glu Trp Thr
67           105                 110                 115
69   gtc gtc ttt gac ctg tcg aat gtg gag ccc aca gag cgc cca aca cgc       619
70   Val Val Phe Asp Leu Ser Asn Val Glu Pro Thr Glu Arg Pro Thr Arg
71           120                 125                 130
73   gcg cgc tta gag ttg cgg ctg gag gct gag tgt gaa gat aca gga ggg       667
74   Ala Arg Leu Glu Leu Arg Leu Glu Ala Glu Cys Glu Asp Thr Gly Gly
75   135                 140                 145                 150
77   tgg gag cta agc gtg gca ctg tgg gcc gac gca gag cat cca ggg cct       715
78   Trp Glu Leu Ser Val Ala Leu Trp Ala Asp Ala Glu His Pro Gly Pro
79                   155                 160                 165
81   gag ctg ctg cgc gtg ccg gcg cca cca ggg gtg ctc ctg cgc gca gac       763
82   Glu Leu Leu Arg Val Pro Ala Pro Pro Gly Val Leu Leu Arg Ala Asp
83                   170                 175                 180
85   cta ctg ggg act gca gta gcc gcc aac gca tca gtg ccc tgt act gtg       811
86   Leu Leu Gly Thr Ala Val Ala Ala Asn Ala Ser Val Pro Cys Thr Val
87           185                 190                 195
89   cgc ctg gcg ctg tca ctg cac cct ggg gcc act gca gcc tgt ggg cgc       859
90   Arg Leu Ala Leu Ser Leu His Pro Gly Ala Thr Ala Ala Cys Gly Arg
91           200                 205                 210
93   ctg gct gag gcc tcc ctg ctg ctg gtg acg ctg gac cca cgc ctg tgt       907
94   Leu Ala Glu Ala Ser Leu Leu Leu Val Thr Leu Asp Pro Arg Leu Cys
95   215                 220                 225                 230
97   ccc ttg ccg cga ttg cgg cgc cac acg gag ccc agg gta gaa gtt ggt       955
98   Pro Leu Pro Arg Leu Arg Arg His Thr Glu Pro Arg Val Glu Val Gly
99                   235                 240                 245
101  cca gtg ggc act tgt cgt acc cga cgg ttg cat gtg agc ttc cgt gag      1003
102  Pro Val Gly Thr Cys Arg Thr Arg Arg Leu His Val Ser Phe Arg Glu
103                  250                 255                 260
105  gtg ggc tgg cac cgt tgg gtg atc gcg ccg cgt ggc ttc cta gcc aac      1051
106  Val Gly Trp His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn
107                  265                 270                 275
109  ttc tgc cag ggc acg tgc gca cta ccc gaa acg ctg agg gga ccc ggc      1099
110  Phe Cys Gln Gly Thr Cys Ala Leu Pro Glu Thr Leu Arg Gly Pro Gly
111          280                 285                 290
113  ggg ccg cct gca ctc aac cac gct gtg ctg cgc gcg ctc atg cac gca      1147
114  Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala
115  295                 300                 305                 310
117  gct gct ccc acc ccg ggt gca ggc tcg ccc tgc tgc gtg cca gag cgt      1195
118  Ala Ala Pro Thr Pro Gly Ala Gly Ser Pro Cys Cys Val Pro Glu Arg
119                  315                 320                 325
121  cta tca ccc atc tcc gtg ctc ttc ttc gac aat agt gac aac gtg gtc      1243
122  Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val
123                  330                 335                 340
125  ctg cga cac tac gaa gac atg gtg gtg gat gag tgt ggc tgc cgt          1288
126  Leu Arg His Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
127                  345                 350                 355
129  tgaccacccg ggacaccctt tcagggaccg ccccacgcaa aagcagggac tgtttgttca    1348
```

RAW SEQUENCE LISTING   DATE: 10/02/2001
PATENT APPLICATION: US/09/756,481A   TIME: 11:48:10

Input Set : A:\47506-sequence.txt
Output Set: N:\CRF3\10022001\I756481A.raw

130   tgttttattg gtgacaaaaa gcttaaaaca aatttgact   1387
132 <210> SEQ ID NO: 2
133 <211> LENGTH: 357
134 <212> TYPE: PRT
135 <213> ORGANISM: Artificial Sequence
W--> 137 <220> FEATURE:
W--> 137 <223> OTHER INFORMATION:
137 <400> SEQUENCE: 2
138   Met Leu Pro Val Cys His Arg Phe Cys Asp His Leu Leu Leu Leu Leu
139   1   5   10   15
140   Leu Leu Pro Ser Thr Thr Leu Ala Pro Ala Pro Ala Ser Met Gly Pro
141   20   25   30
142   Ala Ala Ala Leu Leu Gln Val Leu Gly Leu Pro Glu Ala Pro Arg Ser
143   35   40   45
144   Val Pro Thr His Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg
145   50   55   60
146   Arg Arg Asp Pro Gln Glu Ala Arg Val Gly Arg Pro Leu Arg Pro Cys
147   65   70   75   80
148   His Val Glu Glu Leu Gly Val Ala Gly Asn Ile Val Arg His Ile Pro
149   85   90   95
150   Asp Ser Gly Leu Ser Ser Arg Pro Ala Gln Pro Ala Arg Thr Ser Gly
151   100   105   110
152   Leu Cys Pro Glu Trp Thr Val Val Phe Asp Leu Ser Asn Val Glu Pro
153   115   120   125
154   Thr Glu Arg Pro Thr Arg Ala Arg Leu Glu Leu Arg Leu Glu Ala Glu
155   130   .135   140
157   Cys Glu Asp Thr Gly Gly Trp Glu Leu Ser Val Ala Leu Trp Ala Asp
158   145   150   155   160
159   Ala Glu His Pro Gly Pro Glu Leu Leu Arg Val Pro Ala Pro Pro Gly
160   165   170   175
161   Val Leu Leu Arg Ala Asp Leu Leu Gly Thr Ala Val Ala Ala Asn Ala
162   180   185   190
163   Ser Val Pro Cys Thr Val Arg Leu Ala Leu Ser Leu His Pro Gly Ala
164   195   200   205
165   Thr Ala Ala Cys Gly Arg Leu Ala Glu Ala Ser Leu Leu Leu Val Thr
166   210   215   220
167   Leu Asp Pro Arg Leu Cys Pro Leu Pro Arg Leu Arg Arg His Thr Glu
168   225   230   235   240
169   Pro Arg Val Glu Val Gly Pro Val Gly Thr Cys Arg Thr Arg Arg Leu
170   245   250   255
171   His Val Ser Phe Arg Glu Val Gly Trp His Arg Trp Val Ile Ala Pro
172   260   265   270
173   Arg Gly Phe Leu Ala Asn Phe Cys Gln Gly Thr Cys Ala Leu Pro Glu
174   275   280   285
175   Thr Leu Arg Gly Pro Gly Gly Pro Pro Ala Leu Asn His Ala Val Leu
176   290   295   300
177   Arg Ala Leu Met His Ala Ala Ala Pro Thr Pro Gly Ala Gly Ser Pro
178   305   310   315   320
179   Cys Cys Val Pro Glu Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp

```
180                      325                 330                 335
181   Asn Ser Asp Asn Val Val Leu Arg His Tyr Glu Asp Met Val Val Asp
182               340                 345                 350
183   Glu Cys Gly Cys Arg
184           355
```

VERIFICATION SUMMARY   DATE: 10/02/2001
PATENT APPLICATION: US/09/756,481A   TIME: 11:48:11

Input Set : **A:\47506-sequence.txt**
Output Set: **N:\CRF3\10022001\I756481A.raw**

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:137 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:137 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

STATISTICS SUMMARY   DATE: 10/02/2001
PATENT APPLICATION: US/09/756,481A   TIME: 11:48:11

Input Set : **A:\47506-sequence.txt**
Output Set: **N:\CRF3\10022001\I756481A.raw**

Application Serial Number: US/09/756,481A
Alpha or Numeric: Numeric
Application Class:
Application File Date: 08-30-2001
Art Unit: OIPE
Software Application: FastSeq
Total Number of Sequences: 2
Total Nucleotides: 1387
Total Amino Acids: 357
Number of Errors: 0
Number of Warnings: 3
Number of Corrections: 1

MESSAGE SUMMARY

258 W: 3 (Mandatory Feature missing)
271 C: 1 (Current Filing Date differs)